



SEQ LST.txt
SEQUENCE LISTING

<110> HENRY, JAMES
CAHILL, CATHERINE
YASHPAL, KIRAN

<120> OLIGONUCLEOTIDES AND OTHER MODULATORS OF THE NK-1
RECEPTOR PATHWAY AND THERAPEUTIC USES THEREOF

<130> 457-117us

<140> 09/930,503

<141> 2001-08-16

<150> 60/226,086

<151> 2000-08-18

<160> 60

<170> PatentIn Ver. 2.1

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<211> 311

<212> PRT

<213> Homo sapiens

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Thr Asn Thr Ser Glu Pro Asn Gln Phe Val Gln Pro Ala Trp Gln Ile
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Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val
35 40 45

Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
180 185 190

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Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
 195 200 205
 Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
 210 215 220
 Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
 225 230 235 240
 Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
 245 250 255
 Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
 260 265 270
 Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu
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 ccagctgtga gacaagaggg acaagtgggg actgcagcta acttatcatc acacaactca 1200
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 <213> Homo sapiens

<400> 3
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20 25 30
Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val
35 40 45
Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
50 55 60
Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
65 70 75 80
Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
85 90 95
Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
100 105 110
Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
115 120 125
Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
130 135 140
Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
145 150 155 160
Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
165 170 175
Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
180 185 190
Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
195 200 205
Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
210 215 220
Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
225 230 235 240
Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
245 250 255
Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
260 265 270
Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu
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SEQ LST.txt

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cggaacccaa tcagttcgtg caaccagcct ggcaaattgt cctttgggca gctgcctaca 240
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      20              25              30

Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val
      35              40              45

Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
      50              55              60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
      65              70              75              80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
      85              90              95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
      100              105              110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
      115              120              125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
      130              135              140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
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Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser

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175

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Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
195 200 205
Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
210 215 220
Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
225 230 235 240
Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
245 250 255
Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
260 265 270
Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu
275 280 285
Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile
290 295 300
Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe
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Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met
325 330 335
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Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu
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Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser
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 Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val
 35 40 45
 Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
 50 55 60
 Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
 65 70 75 80
 Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
 85 90 95
 Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
 100 105 110
 Ile Ala Ala Cys Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
 115 120 125
 Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
 130 135 140
 Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
 145 150 155 160
 Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
 165 170 175
 Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr

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180	185	190
Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro		
195	200	205
Leu Leu Val Ile Gly Tyr Ala Tyr Thr Ile Val Gly Ile Thr Leu Trp		
210	215	220
Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val		
225	230	235
Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr		
245	250	255
Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr		
260	265	270
Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu		
275	280	285
Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile		
290	295	300
Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe		
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Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met		
325	330	335
Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser		
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Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu		
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Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser		
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Phe Ser Ser Asn Val Leu Ser		
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 <213> Homo sapiens

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 actgtgctga tctacttcct cccctgctg gtgattggct atgcatacac catagtggga 660
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aaccccat	ca	tctact	gctg	cctcaat	gac	aggttcc	gtc	960
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tatctcca	gag	ggcag	ggag	ccag	ag	gacggc	cc	1080
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<220>
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<400> 11
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<210> 12
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<220>
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<210> 13
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 <400> 27
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<210> 28
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<210> 29

SEQ LST.txt

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 <210> 30
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SEQ LST.txt

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SEQ LST.txt

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